

RAW SEQUENCE LISTING

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Application Serial Number:

10/584,972

Source:

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2-26-05

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RAW SEQUENCE LISTING DATE: 02/26/2005
PATENT APPLICATION: US/10/524,972 TIME: 10:37:39

Input Set : A:\Final sequence list-13173-00007-US.txt
Output Set: N:\CRF4\02262005\J524972.raw

4 <110> APPLICANT: Schopfer, Christel R.
 5 Flachmann, Ralf
 6 Herbers, Karin
 7 Kunze, Irene
 8 Sauer, Matt
 9 Klebsattel, Martin
 11 <120> TITLE OF INVENTION: Method for the production of Astaxanthin in flowers of
 plants
 13 <130> FILE REFERENCE: 13173-00007-US
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/524,972
 C--> 15 <141> CURRENT FILING DATE: 2005-02-18
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/009102
 16 <151> PRIOR FILING DATE: 2003-08-18
 18 <150> PRIOR APPLICATION NUMBER: DE 102 38 980.2
 19 <151> PRIOR FILING DATE: 2002-08-20
 21 <150> PRIOR APPLICATION NUMBER: DE 102 38 978.0
 22 <151> PRIOR FILING DATE: 2002-08-20
 24 <150> PRIOR APPLICATION NUMBER: DE 102 38 979.9
 25 <151> PRIOR FILING DATE: 2002-08-20
 27 <150> PRIOR APPLICATION NUMBER: DE 102 53 112.9
 28 <151> PRIOR FILING DATE: 2002-11-13
 30 <150> PRIOR APPLICATION NUMBER: DE 102 58 971.2
 31 <151> PRIOR FILING DATE: 2002-12-16
 33 <160> NUMBER OF SEQ ID NOS: 172
 35 <170> SOFTWARE: PatentIn version 3.3
 38 <210> SEQ ID NO: 1
 40 <211> LENGTH: 1771
 42 <212> TYPE: DNA
 44 <213> ORGANISM: Haematococcus pluvialis
 46 <220> FEATURE:
 48 <221> NAME/KEY: CDS
 50 <222> LOCATION: (166)..(1155)
 52 <400> SEQUENCE: 1
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 55 aataataaaag agctcaagcg ttttgtgcgcc tcgacgtggc cagtcgtcac tgccttgaac 120
 57 ccgcgcagtct cccggccgcac tgactgcccatagcacagacta gacgatgcagctatca 177
 58 Met Gln Leu Ala
 59 1
 61 gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag 225
 62 Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys
 63 5 10 15 20
 65 gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg 273
 66 Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp
 67 25 30 35

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69	gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg	321
70	Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro	
71	40 45 50	
74	gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc	369
75	Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile	
76	55 60 65	
78	aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac	417
79	Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His	
80	70 75 80	
82	gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg	465
83	Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
84	85 90 95 100	
86	ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc	513
87	Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser	
88	105 110 115	
90	ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca	561
91	Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	
92	120 125 130	
94	ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg	609
95	Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	
96	135 140 145	
98	aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg	657
99	Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
100	150 155 160	
102	tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac	705
103	Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
104	165 170 175 180	
107	cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga	753
108	His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
109	185 190 195	
111	aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg	801
112	Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
113	200 205 210	
115	tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag	849
116	Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln	
117	215 220 225	
119	ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg	897
120	Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	
121	230 235 240	
123	ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc	945
124	Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro	
125	245 250 255 260	
127	cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg	993
128	His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met	
129	265 270 275	
131	aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt	1041
132	Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe	
133	280 285 290	
135	ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc	1089

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136	Leu	Thr	Cys	Tyr	His	Phe	Asp	Leu	His	Trp	Glu	His	Arg	Trp	Pro		
137	295					300				305							
140	tcc	gcc	ccc	tgg	tgg	gag	ctg	ccc	aac	tgc	cgc	cgc	ctg	tct	ggc	cga	1137
141	Phe	Ala	Pro	Trp	Trp	Glu	Leu	Pro	Asn	Cys	Arg	Arg	Leu	Ser	Gly	Arg	
142	310					315				320							
144	ggt	ctg	gtt	cct	gcc	tag	ctggacacac	tgca	gtggc	cctg	gtgc	cca					1185
145	Gly	Leu	Val	Pro	Ala												
146	325																
148	gtgggc	atcg	ttgt	ttgg	cagg	actgg	ttgg	ttgg	ttgg	ttgg	ttgg	ttgg	ttgg	ttgg	ttgg	ttgg	1245
150	gacac	gcgt	tc	atgg	gttacc	ctgt	gttag	ct	ggcc	acta	gggg	gggg	gggg	gggg	gggg	gggg	1305
152	tcgag	catt	ttgc	ccat	ggat	aag	ctgt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	1365
154	acc	cttgc	cg	gag	atgt	catt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	1425
156	tat	cta	at	tt	ctgaa	ggc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1485
158	aagg	gtc	agg	cac	aa	gg	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	1545
160	ggagg	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	gtt	1605
162	agag	ctgc	gt	at	ttt	act	gg	ttt	gg	ttt	gg	ttt	gg	ttt	gg	ttt	1665
164	agata	act	gg	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1725
166	cc	ctgc	cg	ct	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1771
169	<210>	SEQ	ID	NO:	2												
171	<211>	LENGTH:	329														
173	<212>	TYPE:	PRT														
175	<213>	ORGANISM:	Haematococcus	pluvialis													
177	<400>	SEQUENCE:	2														
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180	1					5				10				15			
183	Glu	Ala	Leu	Lys	Glu	Lys	Glu	Lys	Glu	Val	Ala	Gly	Ser	Ser	Asp	Val	
184						20				25				30			
187	Leu	Arg	Thr	Trp	Ala	Thr	Gln	Tyr	Ser	Leu	Pro	Ser	Glu	Glu	Ser	Asp	
188						35				40			45				
191	Ala	Ala	Arg	Pro	Gly	Leu	Lys	Asn	Ala	Tyr	Lys	Pro	Pro	Pro	Ser	Asp	
192						50				55			60				
195	Thr	Lys	Gly	Ile	Thr	Met	Ala	Leu	Arg	Val	Ile	Gly	Ser	Trp	Ala	Ala	
196	65					70				75				80			
199	Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile	Lys	Leu	Pro	Thr	Ser	Leu	Asp	
200						85				90				95			
203	Gln	Leu	His	Trp	Leu	Pro	Val	Ser	Asp	Ala	Thr	Ala	Gln	Leu	Val	Ser	
204						100				105				110			
207	Gly	Thr	Ser	Ser	Leu	Leu	Asp	Ile	Val	Val	Val	Phe	Phe	Val	Leu	Glu	
208						115				120				125			
211	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Thr	His	Asp	Ala	Met	His	Gly	
212						130				135				140			
215	Thr	Ile	Ala	Met	Arg	Asn	Arg	Gln	Leu	Asn	Asp	Phe	Leu	Gly	Arg	Val	
216	145					150				155				160			
219	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	Phe	Asp	Tyr	Asn	Met	Leu	His	Arg	Lys	
220						165				170				175			
223	His	Trp	Glu	His	His	Asn	His	Thr	Gly	Glu	Val	Gly	Lys	Asp	Pro	Asp	
224						180				185				190			
227	Phe	His	Arg	Gly	Asn	Pro	Gly	Ile	Val	Pro	Trp	Phe	Ala	Ser	Phe	Met	
228						195				200				205			

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231 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
232 210 215 220
235 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
236 225 230 235 240
239 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
240 245 250 255
243 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
244 260 265 270
247 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
248 275 280 285
251 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
252 290 295 300
255 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
256 305 310 315 320
259 Leu Ser Gly Arg Gly Leu Val Pro Ala
260 325
264 <210> SEQ ID NO: 3
266 <211> LENGTH: 1662
268 <212> TYPE: DNA
270 <213> ORGANISM: Haematococcus pluvialis
272 <220> FEATURE:
274 <221> NAME/KEY: CDS
276 <222> LOCATION: (168)..(1130)
278 <400> SEQUENCE: 3
279 cggggcaact caagaaaattc aacagctgca agcgccccc agcctcacag cgccaagtga 60
281 gctatcgacg tggttgtgag cgctcgacgt ggtccactga cgggcctgtg agcctctgct 120
283 ctccgtcctc tgccaaatct cgcgtcgffff cctgcctaag tcgaaga atg cac gtc 176
284 Met His Val
285 1
287 gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc 224
288 Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
289 5 10 15
291 agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc 272
292 Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
293 20 25 30 35
295 gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct 320
296 Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
297 40 45 50
299 cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc 368
300 Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
301 55 60 65
303 acc tgg acc gca gtg ttt tta cac gca ata tttcaa atc agg cta ccg 416
304 Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
305 70 75 80
307 aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc 464
308 Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
309 85 90 95
311 cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc 512
312 Gln Leu Leu Gly Gly Ser Ser Leu Leu His Ile Ala Ala Val Phe

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313	100	105	110	115	
315	att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac				560
316	Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp				
317	120	125	130		
319	gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc				608
320	Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu				
321	135	140	145		
323	ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg				656
324	Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met				
325	150	155	160		
327	ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg				704
328	Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly				
329	165	170	175		
331	aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc				752
332	Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe				
333	180	185	190	195	
335	gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg				800
336	Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu				
337	200	205	210		
339	gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat				848
340	Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn				
341	215	220	225		
343	ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc				896
344	Leu Leu Val Phe Met Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu				
345	230	235	240		
347	ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca				944
348	Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala				
349	245	250	255		
351	gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca				992
352	Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala				
353	260	265	270	275	
355	tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg				1040
356	Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp				
357	280	285	290		
359	gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc				1088
360	Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys				
361	295	300	305		
363	cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga				1130
364	Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala				
365	310	315	320		
367	cctggccctt ccgctggta cccagcgctc gcacaagagt gtcatgtac agggtgctgc				1190
369	ggccagtggc agcgcagtgc actctcagcc tgtatgggc taccgctgtc ccactgagca				1250
371	ctgggcatgc cactgagcac tggcgtgtc actgagcaat gggcgtgcta ctgagcaatg				1310
373	ggcgtgtac tgacaatggg cgtgctactg gggctggca gtggcttagga tggagtttga				1370
375	tgcattcagt agcggtgccc aacgtcatgt ggatggtggaa agtgctgagg ggtagggca				1430
377	gccggcattt gagagggcta agttataaat cgcatgctgc tcatgcgcac atatctgcac				1490
379	acagccaggg aaatcccttc gagagtgatt atggacact tgtattggtt tcgtgttatt				1550
381	gttttattca gcagcagtac ttagtgaggg tgagagcagg gtggtagagag tggagtgtgagt				1610
383	gagttatgaac ctggcagcagc aggtgaacag cctgtatga atgactotgt ct				1662

VERIFICATION SUMMARY
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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date